

Replacement Sheet

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1. 'A' Allele, CYP2D6*3, A2637 deletion, Frameshift resulting in zero enzyme activity

FIGURE 6A
Numbering is according to Kimura et al.

111=63-640				2, Tm=61-63C										Wild Type (+)	Mut (+)
CYPwt(+)AZ624,ZZmer,34%5C, 1m=63-54C CYPwt(+)AZ624(A)30-3'NH2	CYPw(+)A2625(A)30-3'NH2	CYPwt(+)A2625b(A)30-3'NH2	CYPw(+)A2625c(A)30-3'NH2	CYPmut(+)A2624,21mer,57%GC, Tm=61-63C	CYPmut(+)A2624(A)30-3'NH2	CYPmut(+)A2625(A)30-3'NH2	CYPmut(+)A2625b(A)30-3'NH2	CYPmut(+)A2625c(A)30-3'NH2	CYPw(+)A2624b(A)30-3'NH2	CYPw(-)A2625(A)30-3'NH2	CYPwt(+)2629a(A)30-3'NH2	CYPwt(+)2629b(A)30-3'NH2	CYPwt(+)2629c(A)30-3'NH2	CCAGCCCAGCC-3'	CCAGCCCAGCC3
3. G C T A A C T G A G C A C G A T G A C C -3 NH2 5. G C T A A C T G A G C A C A G G A T G A C C (A)30-3. NH2	5. CIAACIGAGCACAGGAIGACC(A)30.3 NH2	5. C T A A C T G A G C A C A G G A T G A C (A)30-3' NH2	5- C T A A C T G A G C A C A G G A T G A (A)30-3' NH2	S-GCTAACTGAGCAC - GGATGACC-3'NH2	5-GCTAACTGAGCAC - GGATGACC (A)30-3' NH2	5. C T A A C T G A G C A C . G G A T G A C C (A)30-3' NH2	5'- C T A A C T G A G C A C · G G A T G A C (A)30-3' NH2	5. C T A A C T G A G C A C . G G A T G A (A)30-3' NH2	5- встааства всасавват в (А)30-3' NH2	NH23-(A)30 gaitgactegigtectaetg-5'	5- c t g x g c a c x g g a t g x c (A)30-3' NH2		С 5-х t g a g c a x a g g a t g a x (A)30-3' NH2	5 G C T G G A T G A G C T G C T A A C T G A G C A C G A T G A C C T G G G A C C C A G C C C A G C C .3	5-GCTGGATGAGCTGCTAACTGAGCAC - GGATGACCTGGGACCCAGCCCAGCC
										NH2 :	x= 2-Amino-dA	x= C-5 propynyl-C	-2612 x= C-5 propynyl-C	S. GCTGGATGAG	S'GCTGGATGAG



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	CYPwt(-)B1922,17mer,76%GC, Tm=66C CYPwt(+)B1922- Target	CYPmut(+)B1922,17mer,71%GC, Tm=58-60C CYPmut(-)B1922, Target	TTCGCCCAACGGTCT-3
1934	NH2 3'- G A G G G T G G G G G T C C T G C 5' 5'- C T C C C A C C C C C A G G A C G -3' NH2	5- C T C C C A C C C C C A A G A C G -3' NH2 -1909 NH23- G A G G G T G G G G T T C T G C -5'	5- CCCTTACCCGCATCTCCCACCCCCAGGACGCCCTTTCGCCCCAACGGTCT-3' WIII

'ild Type (+)

CYPmut(+)B1930,17mer,65%GC, Tm=54C CYPwt(-)B1930,17mer,71%GC, Tm=56C |-1909 5- C C C T T A C C C G C A G A C G C C C C T T T C (A)30-3 NH2 CYPmu((+)B1930(A)30-3 NH2 5- C C C T T A C C C G C A T C T C C C A C G C C C C C T T T C G C C C C A A C G G T C T -3 Wild Type (+) 5- C C C T T A C C C G C A T C T C C C A C C C C C A A G A C G C C C C T T T C G C C C C A A C G G T C T -3 Mut (+) CYPwt(-)B1930(A)30-3'NH2 5. C C C A A G A C G C C C C T T T C -3'NH2 NH23'- G G G C C C C G G G G A A A G -5' NH2 3'-(A)30 G G G G C T G C G G G G A A A G -5' B. CYPwt(-)B1930 (C/A to mut at base 13) and

3. 'C' Allele, CYP2D6*9, G2702-A2704 deletion, decreased enzyme activity

T T C C A C T C T C A C C G A C G G T G C C A C -5.
- - C C A C T C T C A C C G A C G G T G C C A C -5. 5- C A G A G A T G G A · · · G G T G A G A G T G (A)30-3' NH2 5'- G

CYPmut(+)C2691,21mer,57%GC, Tm=60C.

CYPmut(+)C2692(A)30-3'NH2 CYPmut(+)C2691(A)30-3'NH2

CYPwt(+)C2691,22mer,55%GC, Tm=60C

CYPwt(+)C2691(A)30-3'NH2 CYPwt(+)C2692(A)30-3'NH2

3-TGACTCCGGAAGGACCGTCTACCTCTTCCAC3-TGACTCCAC33-TGACTCCGGAAGGACCGTCTACCTACCT---CCAC



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CYPmut(+)E3018,19mer, 63%GC, Tm=62C CYPwt(-)E3018,19mer,58%GC, Tm=60 CYPmut(*)G1840(A)30-3'NH2,18mer,61%GC, Tm=57 Wild Type (+) Wild Type (+) CYPwt(+)G1840(A)30-3'NH2,18mer,67%GC, Tm=60 CYPmut(+)E3009,19mer,58%GC,Pred Tm=59C GTGAGCCCATC-3' Mut(+) CYPwt(-)E3009,19mer,53%GC,Pred Tm=57 CYPmut(-)E3018- Target 5-GCTCATGATCCTACCTCCG-3'NH2 CYPmu((+)E3009,19mer,58%GC,Pred
5-TGGGGCCTCATGATCCTACCTCGG(A)30-3'NH2 CYPmu((+)E3009(A)30-3'NH2
5-TGGGGCCTCATGATCCTACATCCGGATGTGCAGCGTGAGCATC-3'
5-TGGGGCCTCCTGCTCATGATCCTACCTACGATGTGCAGCGTGAGCCATC-3' CYPwt(+)E3018- Target CGGATGTGCAGCGTGAGCCCATC.3' 5- C A C T C C T G T G G G T G A T G G (A)30-3 NH2
C C G C C T T C G C C A C T C C G G T G G T G A T G G G C A G A A G G G C A C A A A G C G G G -3
C C G C C T T C G C C A C T C C T G T G G G T G A T G G G C A G A A G G G C A C A A A G C G G G -3 CYPwt(-)E3009(A)30-3'NH2 CYPw(-)G1840(A)30-3'NH2 -3038-Intron Start -3038-Intron Start 5. C C T A C A T C C G G A T G T G C A G .3'
5. C C T A C C T C C G G A T G T G C A G .3 NH2
3. G G A T G G A G G C C T A C A C G T C .5' NH23-GGATGTAGGCCTACACGTC-5-5-CCTACACGTC-5-5-CCTACATCCGGATGTGCAG3 G G G T G A T G G (A)30-3' NH2 CYPmut(+)E3018 (C/T to wt at base 6) NH2 3-(A)30 G T G A G G C A C C C A C T A C C -5' 1 T G T A G G C -5' A. wt Probe - CYPwt(-)E3009 (T/C to mut at base 5) & CYPmut(+)E3009 (C/A to wt at base 15) 5-TGGGGCCTCCTGCTCATGATCCTACATC 5-TGGGGCCTCCTGCTCATGATCCTACCTC 4. 'E' Allele, CYP2D6*7, A3023C, H324P amino acid change resulls in zero enzyme activity NH23.- C G A G T A C T A G G NH23:-(A)30 C G A G T A C T A G G S-CACTCCGGT 1846 5. 'G' Allele, CYP2D6*8, G1846T, Stop codon, zero enzyme activity B. CYPwt(-)E3018 (T/C to mut at base 14) and 5.676(5.676(

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CYPmut(+)T1785,17mer,71%GC, - GGGTGACCGAGGAGGCCGCCTGCCT-3' CYPmut(+)T1785(A)30-3'NH2 CYPmut(+)T1786(A)30-3'NH2 CYPwt(+)T1786(A)30-3'NH2 CYPwt(+)T1785(A)30-3'NH2 5- G C T G G A G C A G T G G G T G A C (A)30-3' NH2 5- C T G G A G C A G T G G G T G A C (A)30-3' NH2 - G G G T G A C (A)30-3' NH2 5- C T G G A G C A G - G G G T G A C (A)30-3' NH2 5. G C T G G A G C A G . G G G T G A C .3 NH2 5. G C T G G A G C A G . G G G T G A C (A)30.3 5. GGGCAAGAGTCGCTGGAGCAG

Wild Type (+)

(+) Mrt (+)

region somewhere between the PCR primers were it would be easy to discriminate between 206 and its two pseudogenes, 207 and 208. 7. 2D6/2D7/2D8 Controls - The 2D6/7/8 probes were designed in the 1600 region of the 2D6 gene. The purpose of the designs was to find The purpose of the designs is to demonstrate that the PCR amplicon is from the 2D6 gene, not one of the pseudogenes.

CYP2D8wt(+)1607b(A)30-3'NH2 CYP2D8wt(+)1607(A)30-3'NH2 CYP2D7wt(+)1607(A)30-3'NH2 CYP2D6wt(+)1607(A)30-3'NH2 GGAGACCTTGTGGAGCGCCAGGGTTGGAGTGGGTGGC3 GGAGACCAGGAAAAGC - ACAGGGTTGGAGTGGGCGGC3 GGGAGACCAGGGGAGC.ATAGGGTTGGAGTGGGTGGT3 5- G A C C A G G A A A G C - A C A G G G (A)30-3' NH2 5. G A C C A G G G G G A G C . A T A G G (A)30-3" NH2 5. G A C C T T G T G G A G C G C C A G (A)30-3" NH2 5. G A C C A G G A A A A G C . A C A G G (A)30-3" NH2 5 5 5 6 Ö ັດ

8. Pos/Neg Control probes- These probes were designed as true positive and negative control probes. They consist of the same semi-random sequence, with the positive control probe having a 5' Biotin.

CYP(+)ran(A)25-5'Biotin,3'NH2 CYP(+)ran(A)25-3'NH2

CYPwt(+)T1785,18mer,67%GC, Tm=59-61C

5'. G C T G G A G C A G T G G G T G A C -3'NH2

T. Allele, CYP2D6*6, T1795 deletion, Frameshift resulting in zero enzyme activity

FIGURE 6D